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RAW SEQUENCE LISTING
PATENT APPLICATION: -US/10/042,431

DATE: 01/27/2002
TIME: 15:34:20

Input Set : A:\101476ul.app
Output Set: N:\CRF3\01272002\J042431.raw

ENTERED

3 <110> APPLICANT: MCCARTHY, Sean A
4 BARNES, Thomas M
5 FRASER, Christopher C
6 SHARP, John D
8 <120> TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
9 PREVENTIVE, THERAPEUTIC, AND OTHER USES
11 <130> FILE REFERENCE: 10147-6U2
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/042,431
14 <141> CURRENT FILING DATE: 2001-10-25
16 <150> PRIOR APPLICATION NUMBER: US 09/333,159
17 <151> PRIOR FILING DATE: 1999-06-14
19 <150> PRIOR APPLICATION NUMBER: US 09/578,063
20 <151> PRIOR FILING DATE: 2000-05-24
22 <160> NUMBER OF SEQ ID NOS: 79
24 <170> SOFTWARE: PatentIn Ver. 2.1
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27 <211> LENGTH: 1656
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
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34 cccggacccg agtgtttcac agccaatggt gcggattata ggggaacaca gaactggaca 180
35 gcaactacaag gcgggaagcc atgtctgttt tggaacgaga ctttccagca tccatacaac 240
36 actctgaaat accccaacgg ggagggggggc ctgggtgagc acaactattg cagaaatcca 300
37 gatggagacg tgagccctg gtgctatgtg gcagagcacg aggatgggtg ctactggaag 360
38 tactgtgaga tacctgcttg ccagatgcct ggaaacctg gctgctacaa ggatcatgga 420
39 aaccacctc ctctaactgg caccagtaaa acgtccaaca aactcaccat acaaacttgc 480
40 atcagttttt gtcggagtca gaggttcaag tttgctggga tggagtcagg ctatgcttgc 540
41 ttctgtggaa acaatcctga ttactggaag tacggggagg cagccagtag cgaatgcaac 600
42 agcgtctgct tcggggatca caccacaacc tgtggtggcg atggcaggat catcctcttt 660
43 gatactctcg tgggcgcctg cgggtgggaac tactcagcca tgtcttctgt ggtctattcc 720
44 cctgacttcc ccgacaccta tgccacgggg agggctctgct actggaccat ccgggttccg 780
45 ggggcctccc acatccaact cagcttcccc ctatttgaca tcagggactc ggcgacatg 840
46 gtggagcttc tggatggcta caccacccgt gtcctagccc gcttccacgg gaggagccgc 900
47 ccacctctgt ccttcaacgt ctctctggac ttctgcatct tgtatttctt ctctgatgc 960
48 atcaatcagg ccaggggatt tgctgtttta taccaagccg tcaaggaaga actgccacag 1020
49 gagaggcccg ctgtcaacca gacggtggcc gaggtgatca cggagcaggc caacctcagt 1080
50 gtcagcgctg ccgggtcctc caaagtcttc tatgtcatca ccaccagccc cagccacca 1140
51 cctcagactg tcccaggtag caattcctgg gcgcacccca tgggggctgg aagccacaga 1200
52 gttgaaggat ggacagtcta tgggtctggca actctcctca tctcagcatt 1260
53 gtagcaaga tacttctgca cgtcacattc aaatcccatc gtgttctctg ttcaggggac 1320
54 cttagggatt gtcatcaacc agggacttgc ggggaaatct ggagcatttt ttacaagcct 1380

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55 tccacttcaa tttccatctt taagaagaaa ctcaagggtc agagtcaaca agatgaccgc 1440
56 aatcccccttg tgagtgacta aaaaccccac tgtgcctagg acttgaggtc cctctttgag 1500
57 ctcaaggctg cgtgggtcaa cctctcctgt ggttcttctc tgacagactc tcccctctc 1560
58 tccctctgcc tcggcctctt cggggaaacc ctctcctac agactaggaa gaggcacctg 1620
59 ctgccagggc aggcagagcc tggattcctc ctgctt 1656
62 <210> SEQ ID NO: 2
63 <211> LENGTH: 1425
64 <212> TYPE: DNA
65 <213> ORGANISM: Homo sapiens
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69 cggcccgccgc ctagccccc cctcgccccc ggaccgaggt gttcacagc caatggtgcg 120
70 gattataggg gaacacagaa ctggacagca ctacaaggcg ggaagccatg tctgttttg 180
71 aacgagactt tccagcatcc atacaacact ctgaaatacc ccaacgggga ggggggctg 240
72 ggtgagcaca actattgcag aaatccagat ggagacgtga gcccctggtg ctatgtggca 300
73 gagcagcagg atggtgtcta ctggaagtac tgtgagatac ctgcttgcca gatgcctgga 360
74 aaccttggtt gctacaagga tcatggaaac ccacctcctc taactggcac cagtaaaacg 420
75 tccaacaaac tcaccataca aacttgcatc agtttttgtc ggagtcagag gttcaagttt 480
76 gctgggatgg agtcaggcta tgcttgcttc tgtggaaaca atcctgatta ctggaagtac 540
77 ggggaggcag ccagtaccga atgcaacagc gtctgcttcg gggatcacac ccaaccctgt 600
78 ggtggcgatg gcaggatcat cctctttgat actctcgttg gcgcctgcgg tgggaactac 660
79 tcagccatgt cttctgtggt ctattccctt gacttccccg acacctatgc cacggggagg 720
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82 ctagcccgct tcacggggag gagccgccc cctctgtcct tcaacgtctc tctggacttc 900
83 gtcactctgt atttcttctc tgatcgcatc aatcaggccc agggatttgc tgttttatac 960
84 caagccgtca aggaagaact gccacaggag aggccgctg tcaaccagac ggtggccgag 1020
85 gtgatcacgg agcaggccaa cctcagtgtc agcgtgccc ggtcctccaa agtctcttat 1080
86 gtcacacca ccagccccag ccaccacact cagactgtcc caggtagcaa ttcctgggag 1140
87 ccacccatgg ggcctggaag ccacagagtt gaaggatgga cagtctatgg tctggcaact 1200
88 ctctcatcc tcacagtcac agccattgta gcaaagatac ttctgcacgt cacattcaaa 1260
89 tccatcgtg ttctgtcttc agggacatt agggattgtc atcaaccagg gacttcgggg 1320
90 gaaatctgga gcatttttta caagccttc acttcaattt ccatctttaa gaagaaactc 1380
91 aagggtcaga gtcaacaaga tgaccgcaat ccccttgtga gtgac 1425
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95 <211> LENGTH: 475
96 <212> TYPE: PRT
97 <213> ORGANISM: Homo sapiens
99 <400> SEQUENCE: 3
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101 1 5 10 15
103 Thr Leu Ala Ala Arg Pro Ala Pro Ser Pro Gly Leu Gly Pro Gly Pro
104 20 25 30
106 Glu Cys Phe Thr Ala Asn Gly Ala Asp Tyr Arg Gly Thr Gln Asn Trp
107 35 40 45
109 Thr Ala Leu Gln Gly Gly Lys Pro Cys Leu Phe Trp Asn Glu Thr Phe
110 50 55 60
112 Gln His Pro Tyr Asn Thr Leu Lys Tyr Pro Asn Gly Glu Gly Gly Leu
113 65 70 75

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115 Gly Glu His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Ser Pro Trp
116                               85                               90
118 Cys Tyr Val Ala Glu His Glu Asp Gly Val Tyr Trp Lys Tyr Cys Glu
119                               100                               105
121 Ile Pro Ala Cys Gln Met Pro Gly Asn Leu Gly Cys Tyr Lys Asp His
122                               115                               120
124 Gly Asn Pro Pro Pro Leu Thr Gly Thr Ser Lys Thr Ser Asn Lys Leu
125                               130                               135
127 Thr Ile Gln Thr Cys Ile Ser Phe Cys Arg Ser Gln Arg Phe Lys Phe
128 145                               150                               155
130 Ala Gly Met Glu Ser Gly Tyr Ala Cys Phe Cys Gly Asn Asn Pro Asp
131                               165                               170
133 Tyr Trp Lys Tyr Gly Glu Ala Ala Ser Thr Glu Cys Asn Ser Val Cys
134                               180                               185
136 Phe Gly Asp His Thr Gln Pro Cys Gly Gly Asp Gly Arg Ile Ile Leu
137                               195                               200
139 Phe Asp Thr Leu Val Gly Ala Cys Gly Gly Asn Tyr Ser Ala Met Ser
140                               210                               215
142 Ser Val Val Tyr Ser Pro Asp Phe Pro Asp Thr Tyr Ala Thr Gly Arg
143 225                               230                               235
145 Val Cys Tyr Trp Thr Ile Arg Val Pro Gly Ala Ser His Ile His Phe
146                               245                               250
148 Ser Phe Pro Leu Phe Asp Ile Arg Asp Ser Ala Asp Met Val Glu Leu
149                               260                               265
151 Leu Asp Gly Tyr Thr His Arg Val Leu Ala Arg Phe His Gly Arg Ser
152                               275                               280
154 Arg Pro Pro Leu Ser Phe Asn Val Ser Leu Asp Phe Val Ile Leu Tyr
155                               290                               295
157 Phe Phe Ser Asp Arg Ile Asn Gln Ala Gln Gly Phe Ala Val Leu Tyr
158 305                               310                               315
160 Gln Ala Val Lys Glu Glu Leu Pro Gln Glu Arg Pro Ala Val Asn Gln
161                               325                               330
163 Thr Val Ala Glu Val Ile Thr Glu Gln Ala Asn Leu Ser Val Ser Ala
164                               340                               345
166 Ala Arg Ser Ser Lys Val Leu Tyr Val Ile Thr Thr Ser Pro Ser His
167                               355                               360
169 Pro Pro Gln Thr Val Pro Gly Ser Asn Ser Trp Ala Pro Pro Met Gly
170                               370                               375
172 Ala Gly Ser His Arg Val Glu Gly Trp Thr Val Tyr Gly Leu Ala Thr
173 385                               390                               395
175 Leu Leu Ile Leu Thr Val Thr Ala Ile Val Ala Lys Ile Leu Leu His
176                               405                               410
178 Val Thr Phe Lys Ser His Arg Val Pro Ala Ser Gly Asp Leu Arg Asp
179                               420                               425
181 Cys His Gln Pro Gly Thr Ser Gly Glu Ile Trp Ser Ile Phe Tyr Lys
182                               435                               440
184 Pro Ser Thr Ser Ile Ser Ile Phe Lys Lys Lys Leu Lys Gly Gln Ser
185                               450                               455
187 Gln Gln Asp Asp Arg Asn Pro Leu Val Ser Asp

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188 465
191 <210> SEQ ID NO: 4
192 <211> LENGTH: 19
193 <212> TYPE: PRT
194 <213> ORGANISM: Homo sapiens
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198 1 5 10 15
200 Thr Leu Ala
204 <210> SEQ ID NO: 5
205 <211> LENGTH: 456
206 <212> TYPE: PRT
207 <213> ORGANISM: Homo sapiens
209 <400> SEQUENCE: 5
210 Ala Arg Pro Ala Pro Ser Pro Gly Leu Gly Pro Gly Pro Glu Cys Phe
211 1 5 10 15
213 Thr Ala Asn Gly Ala Asp Tyr Arg Gly Thr Gln Asn Trp Thr Ala Leu
214 20 25 30
216 Gln Gly Gly Lys Pro Cys Leu Phe Trp Asn Glu Thr Phe Gln His Pro
217 35 40 45
219 Tyr Asn Thr Leu Lys Tyr Pro Asn Gly Glu Gly Gly Leu Gly Glu His
220 50 55 60
222 Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Ser Pro Trp Cys Tyr Val
223 65 70 75 80
225 Ala Glu His Glu Asp Gly Val Tyr Trp Lys Tyr Cys Glu Ile Pro Ala
226 85 90 95
228 Cys Gln Met Pro Gly Asn Leu Gly Cys Tyr Lys Asp His Gly Asn Pro
229 100 105 110
231 Pro Pro Leu Thr Gly Thr Ser Lys Thr Ser Asn Lys Leu Thr Ile Gln
232 115 120 125
234 Thr Cys Ile Ser Phe Cys Arg Ser Gln Arg Phe Lys Phe Ala Gly Met
235 130 135 140
237 Glu Ser Gly Tyr Ala Cys Phe Cys Gly Asn Asn Pro Asp Tyr Trp Lys
238 145 150 155 160
240 Tyr Gly Glu Ala Ala Ser Thr Glu Cys Asn Ser Val Cys Phe Gly Asp
241 165 170 175
243 His Thr Gln Pro Cys Gly Gly Asp Gly Arg Ile Ile Leu Phe Asp Thr
244 180 185 190
246 Leu Val Gly Ala Cys Gly Gly Asn Tyr Ser Ala Met Ser Ser Val Val
247 195 200 205
249 Tyr Ser Pro Asp Phe Pro Asp Thr Tyr Ala Thr Gly Arg Val Cys Tyr
250 210 215 220
252 Trp Thr Ile Arg Val Pro Gly Ala Ser His Ile His Phe Ser Phe Pro
253 225 230 235 240
255 Leu Phe Asp Ile Arg Asp Ser Ala Asp Met Val Glu Leu Leu Asp Gly
256 245 250 255
258 Tyr Thr His Arg Val Leu Ala Arg Phe His Gly Arg Ser Arg Pro Pro
259 260 265 270
261 Leu Ser Phe Asn Val Ser Leu Asp Phe Val Ile Leu Tyr Phe Phe Ser

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262      275      280      285
264 Asp Arg Ile Asn Gln Ala Gln Gly Phe Ala Val Leu Tyr Gln Ala Val
265      290      295      300
267 Lys Glu Glu Leu Pro Gln Glu Arg Pro Ala Val Asn Gln Thr Val Ala
268 305      310      315      320
270 Glu Val Ile Thr Glu Gln Ala Asn Leu Ser Val Ser Ala Ala Arg Ser
271      325      330      335
273 Ser Lys Val Leu Tyr Val Ile Thr Thr Ser Pro Ser His Pro Pro Gln
274      340      345      350
276 Thr Val Pro Gly Ser Asn Ser Trp Ala Pro Pro Met Gly Ala Gly Ser
277      355      360      365
279 His Arg Val Glu Gly Trp Thr Val Tyr Gly Leu Ala Thr Leu Leu Ile
280      370      375      380
282 Leu Thr Val Thr Ala Ile Val Ala Lys Ile Leu Leu His Val Thr Phe
283 385      390      395      400
285 Lys Ser His Arg Val Pro Ala Ser Gly Asp Leu Arg Asp Cys His Gln
286      405      410      415
288 Pro Gly Thr Ser Gly Glu Ile Trp Ser Ile Phe Tyr Lys Pro Ser Thr
289      420      425      430
291 Ser Ile Ser Ile Phe Lys Lys Lys Leu Lys Gly Gln Ser Gln Gln Asp
292      435      440      445
294 Asp Arg Asn Pro Leu Val Ser Asp
295      450      455
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299 <211> LENGTH: 373
300 <212> TYPE: PRT
301 <213> ORGANISM: Homo sapiens
303 <400> SEQUENCE: 6
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307 Thr Ala Asn Gly Ala Asp Tyr Arg Gly Thr Gln Asn Trp Thr Ala Leu
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310 Gln Gly Gly Lys Pro Cys Leu Phe Trp Asn Glu Thr Phe Gln His Pro
311      35      40      45
313 Tyr Asn Thr Leu Lys Tyr Pro Asn Gly Glu Gly Gly Leu Gly Glu His
314      50      55      60
316 Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Ser Pro Trp Cys Tyr Val
317 65      70      75      80
319 Ala Glu His Glu Asp Gly Val Tyr Trp Lys Tyr Cys Glu Ile Pro Ala
320      85      90      95
322 Cys Gln Met Pro Gly Asn Leu Gly Cys Tyr Lys Asp His Gly Asn Pro
323      100      105      110
325 Pro Pro Leu Thr Gly Thr Ser Lys Thr Ser Asn Lys Leu Thr Ile Gln
326      115      120      125
328 Thr Cys Ile Ser Phe Cys Arg Ser Gln Arg Phe Lys Phe Ala Gly Met
329      130      135      140
331 Glu Ser Gly Tyr Ala Cys Phe Cys Gly Asn Asn Pro Asp Tyr Trp Lys
332 145      150      155      160
334 Tyr Gly Glu Ala Ala Ser Thr Glu Cys Asn Ser Val Cys Phe Gly Asp

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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number